

CLAIMS

WHAT IS CLAIMED IS:

1. An isolated nucleic acid fragment comprising a nucleic acid sequence encoding a fatty acid hydroxylase with an amino acid identity of 60% or greater to the polypeptide encoded by SEQ ID NO:4.
2. The isolated nucleic acid fragment of Claim 1, wherein the amino acid identity is 90% or greater to the polypeptide encoded by SEQ ID NO:4.
3. The isolated nucleic acid fragment of Claim 1, wherein the amino acid identity is 100% of the polypeptide encoded by SEQ ID NO:4.
4. An isolated nucleic acid fragment having a nucleic acid identity of 90% or greater of a nucleotide sequence of SEQ ID NO:1, 2, or 3.
5. An isolated nucleic acid having a nucleotide sequence of SEQ ID NO:1, SEQ ID NO:2 or SEQ ID NO:3.
6. The isolated nucleic acid fragment of Claim 1, wherein said fragment is isolated from an oil-producing plant species.

7. A chimeric gene capable of causing altered levels of ricinoleic acid in a transformed plant cell, said chimeric gene comprising a nucleic acid fragment of Claim 1, said fragment operably linked to suitable regulatory sequences.

8. A chimeric gene capable of causing altered levels of lesquerolic acid in a transformed plant cell, said chimeric gene comprising a nucleic acid fragment of Claim 1, said fragment operably linked to suitable regulatory sequences.

9. A chimeric gene capable of causing altered levels of fatty acids in a transformed plant cell, said chimeric gene comprising a nucleic acid fragment of Claim 1, said fragment operably linked to suitable regulatory sequences.

10. A chimeric gene capable of causing altered levels of fatty acids in a transformed plant cell, said chimeric gene comprising a nucleic acid fragment of Claim 2, said fragment operably linked to suitable regulatory sequences.

11. A chimeric gene capable of causing altered levels of fatty acids in a transformed plant cell, said chimeric gene comprising a

nucleic acid fragment of Claim 4, said fragment operably linked to suitable regulatory sequences.

12. Plants containing the chimeric gene of any one of claims 7, 8, 9, 10 or 11.

13. Oil obtained from seeds of the plants of claim 12.

14. The isolated nucleic acid fragment of Claim 1, wherein said fragment is obtainable from *Ricinus communis* (L.) (Castor).

15. The isolated nucleic acid fragment of Claim 1, wherein said fragment is obtainable from *Lesquerella fendleri*.

16. A method of producing seed oil containing altered levels of hydroxylated fatty acids comprising:

(a) transforming a plant cell of an oil-producing species with a chimeric gene containing an isolated nucleic acid of Claim 1;

(b) growing fertile plants from the transformed plant cells of step (a);

(c) screening progeny seeds from the fertile plants of step (b) for the desired levels of hydroxylated fatty acids; and

(d) processing the progeny seed of step (c) to obtain seed oil containing altered levels of hydroxylated fatty acids.

17. The method of Claim 16, wherein said plant is selected from the group consisting of rapeseed, Crambe, *Brassica juncea*, Canola, flax, sunflower, safflower, cotton, cuphea, soybean, peanut, coconut, oil palm and corn.

18. A method of producing seed oil containing altered levels of hydroxylated fatty acids comprising:

(a) transforming a plant cell of an oil-producing species with a chimeric gene containing the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:2 or SEQ ID NO:3;

(b) growing fertile plants from the transformed plant cells of step (a);

(c) screening progeny seeds from the fertile plants of step (b) for the desired levels of hydroxylated fatty acids; and

(d) processing the progeny seed of step (c) to obtain seed oil containing altered levels of unsaturated fatty acids.

19. The method of Claim 18, wherein said plant is selected from the group consisting of

rapeseed, Crambe, *Brassica juncea*, Canola, flax, sunflower, safflower, cotton, cuphea, soybean, peanut, coconut, oil palm and corn.

20. A triglyceride oil from a plant selected from the group consisting of rapeseed, Crambe, *Brassica juncea*, Canola, flax, sunflower, cotton, cuphea, soybean, peanut, coconut, oil palm and corn, wherein the fatty acid composition of the oil has been modified to contain hydroxylated fatty acids by a method comprising growing a plant cell having integrated in its genome a DNA construct containing a plant hydroxylase encoding sequence of Claim 1, under conditions which will permit the transcription and translation of said plant hydroxylase in the plant cells.

21. A method to isolate nucleic acid fragments encoding fatty acid hydroxylases comprising:

(a) comparing SEQ ID NO:4 and other fatty acid hydroxylase sequences and fatty acid desaturases;

(b) identifying conserved sequences of 4 or more amino acids obtained in step (a);

(c) designing degenerate oligomers based on the conserved sequences identified in step (b);

(d) using the degenerate oligomers of step

(c) to isolate sequences encoding fatty acid hydroxylases by sequence dependent protocols;

(e) obtaining the deduced amino acid sequence of the encoded gene product from the nucleotide sequence of the gene and;

(f) distinguishing hydroxylase genes from desaturase genes by analyzing amino acid sequence differences between fatty acid desaturases and fatty acid hydroxylases.

22. A method of producing seed oil containing altered levels of unsaturated fatty acids comprising:

(a) transforming a plant cell of an oil-producing species with a chimeric gene containing an isolated nucleic acid comprising a nucleic acid sequence encoding a fatty acid hydroxylase with an amino acid identity of 60% or greater to the polypeptide encoded by SEQ ID NO:4;

(b) growing fertile plants from the transformed plant cells of step (a);

(c) screening progeny seeds from the fertile plants of step (b) for the desired levels of unsaturated fatty acids; and

(d) processing the progeny seed of step (c) to obtain seed oil containing altered levels of unsaturated fatty acids.

23. A chimeric gene capable of causing altered levels of oleic acid in a transformed plant cell, said chimeric gene comprising a nucleic acid sequence encoding a fatty acid hydroxylase with an amino acid identity of 60% or greater to the polypeptide encoded by SEQ ID NO:4 and operably linked to regulatory sequences.

24. A chimeric gene capable of causing altered levels of oleic acid in a transformed plant cell, said chimeric gene comprising a nucleic acid sequence encoding a fatty acid hydroxylase with an amino acid identity of 60% or greater to the polypeptide encoded by SEQ ID NO:4 in which directed changes have been made which lead to the replacement of one or more essential histidine residues in the corresponding gene product, said chimeric gene operably linked to regulatory sequences.

25. The method of Claims 22, 23 or 24, wherein said plant is selected from the group consisting of rapeseed, Crambe, *Brassica juncea*, Canola, flax, sunflower, safflower, cotton, cuphea, soybean, peanut, coconut, oil palm and corn.